

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAygaWej: 995 aa
>SEQ ID NO:2
vs /tmp/fastaDAAzgaWej library
searching /tmp/fastaDAAzgaWej library

1008 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 39, opt: 27, gap-pen: -12/ -2, width: 16
Scan time: 0.034

The best scores are: opt
M13699 ACCESSION:M13699 NID: gi 180255 gb M13699. (1008) 2671

>>M13699 ACCESSION:M13699 NID: gi 180255 gb M13699.1 HUM (1008 aa)
initn: 1414 init1: 972 opt: 2671
Smith-Waterman score: 3980; 57.002% identity in 1014 aa overlap (1-992:1-1008)

	10	20	30	40	50	
SEQ	MKILILGIFLFLC	SSPGWAIDRH	CYIGIEESI	WNYAPSG	KNMLNEK	PFSEDL-----FLQ

M13699	MKILILGIFLFLC	STPAWAKEKH	YIIGIET	TWDYA---	SDHGEKK	LISVDTEHSNIYLQ
	10	20	30	40	50	
	60	70	80	90	100	110
SEQ	GGQARKSFVFK	KALYFQYTD	NTFQRIIE	KPSWLGFL	GPMIKAET	GDFIYVHVKNNASRAY
	..	:	:	:	:	:
M13699	NGPDRIGRLYK	KALYLQYTD	ETFRTTIE	KPVWLGFL	GPIIKAET	GDKVYVHLKNLASRPY
	60	70	80	90	100	110
	120	130	140	150	160	170
SEQ	SYHPHGLTYSK	ENEAHGA	IYPDNTT	GLQKEVE	YLEPGKQ	YTYKWVVEEHQGP

M13699	TFHSHGITYYK	EHE--GA	IYPDNTT	DFQRADD	KVYPGEQ	TYMLLATEEQSP
	120	130	140	150	160	170
	180	190	200	210	220	230
SEQ	TRIVHSHIDT	ARDVASGL	IGPILTC	KRGTLNG	DTEKDID	RSSFLMFSTDES

M13699	TRIVHSHIDAP	KDIASGL	IGPLICK	KDSLDEK	EKHIDRE	FVVMFSVVDEN
	180	190	200	210	220	230
	240	250	260	270	280	290
SEQ	IRAF-TESG	KINTSDP	RFEESMS	MQSINGY	IYGNL	PNLTMCAEDRV

M13699	IKTYCSEPEK	VDKDNED	FQESNR	MYSVNGY	TFGSLP	GLSMCAEDRV
	240	250	260	270	280	290
	300	310	320	330	340	350
SEQ	PVYLRGQTL	ISRNHRK	DTIMLF	PSSLEDA	FMVAKA	PGVWMLGCQ---

M13699	AAFFHGGAL	TNKNYR	IDTINLF	PATLFD	AYMVAQ	NPGEWMLSCQ
	300	310	320	330	340	350

	360	370	380	390	400	410
SEQ	NCQKPST	EAFTGTH	VIHYIIAA	KEILWNYA	PSGIDFF	TKKNLTAAGSKSQLFFERSPTR
	:	:
M13699	ECNKSSSK	DNIRGKH	VRHYIIAA	EEIIWNYA	PSGIDIFT	KENLTAPGSDSAVFFEQGTTR
	360	370	380	390	400	410

	420	430	440	450	460
SEQ	IGGTYKK	LIYREYTD	ASFQTQKAR---	EEHLGILGPV	FKAEVGQTIKITFYNNASLPLSI
	:	:
M13699	IGGSYKK	LVYREYTD	ASFQTNRK	ERGPEEEHL	GILGPVIAEVGDTIRVTFHNKGAYPLSI
	420	430	440	450	460

	470	480	490	500	510	520
SEQ	QPPGLHY	NKSNEGLF	YETP	GGSTPP	SSHVSPGTT	FVYTWEVPKDVGPTSTDPNCL
	:	:	:
M13699	EPIGVRF	NKNNEGTY	YSPNYP	QSRSVPP	SASHVAPT	TETFTYEWTPKEVGPTNADPVCL
	480	490	500	510	520	530

	530	540	550	560	570	580
SEQ	TWFFYSS	VNGKKDIN	SGLLGPLL	ICRNGSL	GDDGKQK	GVDKEFYLLATIFDENESNLLDE
	:	:	:
M13699	AKMYSAV	DPDKIFT	GLIGPMK	ICKKGS	LHANGRQK	DVDKEFYLFPTVFDENESLLED
	540	550	560	570	580	590

	590	600	610	620	630	640
SEQ	N-RTFITE	PENIDKED	TDQASNK	MYSGYMG	NLPGLDTC	LGDNVLWHVFSVGSVEDL
	:	:	:	:	:
M13699	NIRMF	TTAPDQV	DKEDDFQ	ESNKMHS	MNGFMYG	NQPGLTMCCKGDSVVWYLF
	600	610	620	630	640	650

	650	660	670	680	690	700
SEQ	HGIYFSG	NTFTSLG	ARRDTIP	MFYTSQT	LLMTPDS	IGTFDLVCMTIKHNLGGMKHKYHV
	:	:	:	:
M13699	HGIYFSG	NTYLWRG	ERRDTAN	LF	PQTS	LTLMWPDTEGTFNVECLTTDHYTGGMKQKYTV
	660	670	680	690	700	710

	710	720	730	740	750	760
SEQ	RQCGKPN	PDQTYQ	EEKIIIT	IAAEE	MEWDYSP	SRKWENELHHLRRENQTS
	:	:	:	:	:
M13699	NQCR	RQSED	STFYLG	ERTYY-	IAAVE	VEWDYSPQREWEKELHHLQEQNV
	720	730	740	750	760	770

	770	780	790	800	810	820
SEQ	LGSKYK	KVLYRQ	YDDNTFT	NQTKRNE	GEKHL	DILGPLILLNPGQIIQIIFKNKAARPYSI
	:	:	:	:
M13699	IGSKYK	KVVYRQ	YTDSTF	RV	VERKAE	EEHLGILGPQLHADVGDKVKIIFKNMATRPYSI
	780	790	800	810	820	830

	830	840	850	860	870	880
SEQ	HAHG	VKT	MNSTV	VPTQ	PEIQI	YTQIPDR
	:	:	:	:
M13699	HAHG	VQTES	STVPT	LPGET	LT	YVWKIPERSGAGTEDSACIPWAYYSTVDQVKDLYSGLI
	840	850	860	870	880	890

